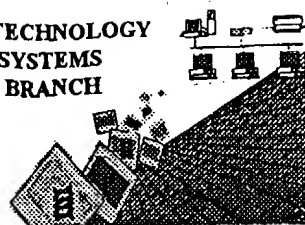


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/635,974

Source:

1600,

Date Processed by STIC:

8/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/635,974

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/635,974

DATE: 05/21/2004

TIME: 16:56:10

Input Set : A:\SeqListing.txt

Output Set: N:\CRF4\05212004\I635974.raw

3 <110> APPLICANT: ImClone Systems Incorporated
W--> 4 <120> TITLE OF INVENTION: Treatment of Hyperproliferative Diseases With Epidermal
W--> 5 Growth Factor Receptor Antagonists
W--> 6 <130> FILE REFERENCE: 11245/48601
W--> 7 <140> CURRENT APPLICATION NUMBER: 09/635,974
C--> 8 <141> CURRENT FILING DATE: 2000-08-09
10 <160> NUMBER OF SEQ ID NOS: 12
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
14 <211> LENGTH: 15
15 <212> TYPE: DNA
16 <213> ORGANISM: Mouse
18 <400> SEQUENCE: 1
E--> 20 aac.tat.ggt.gta.acac
42 <210> SEQ ID NO: 4
43 <211> LENGTH: 15
44 <212> TYPE: PRT
45 <213> ORGANISM: Mouse
47 <400> SEQUENCE: 4
49 Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
E--> 50 1 5 10 15
62 <210> SEQ ID NO: 6
63 <211> LENGTH: 11
64 <212> TYPE: PRT
65 <213> ORGANISM: Mouse
67 <400> SEQUENCE: 6
69 Ala Leu Thr Tyr Asp Tyr Glu Phe Ala Tyr
E--> 70 1 5 10
83 <210> SEQ ID NO: 8
84 <211> LENGTH: 11
85 <212> TYPE: PRT
86 <213> ORGANISM: Mouse
88 <400> SEQUENCE: 8
90 Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
E--> 91 1 5 10
104 <210> SEQ ID NO: 10
105 <211> LENGTH: 6
106 <212> TYPE: PRT
107 <213> ORGANISM: Mouse

Does Not Comply
Corrected Diskette Needed

Found 16
Please group nucleotide bases in groups of 10.
15-16

↓ Pls see item # 3 on error summary sheet.

For ex: aatggtaggaa ^{Insert space} atgaa

RAW SEQUENCE LISTING

DATE: 05/21/2004

PATENT APPLICATION: US/09/635,974

TIME: 16:56:10

Input Set : A:\SeqListing.txt

Output Set: N:\CRF4\05212004\I635974.raw

109 <400> SEQUENCE: 10

111 Ala Ser Glu Ser Ile Ser

E--> 112 1 *S*

125 <210> SEQ ID NO: 12

126 <211> LENGTH: 9

127 <212> TYPE: PRT

128 <213> ORGANISM: Mouse

130 <400> SEQUENCE: 12

132 Gln Gln Asn Asn Asn Trp Pro Thr Thr

E--> 133 1 *S*

VERIFICATION SUMMARY

DATE: 05/21/2004

PATENT APPLICATION: US/09/635,974

TIME: 16:56:11

Input Set : A:\SeqListing.txt

Output Set: N:\CRF4\05212004\I635974.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
 L:6 M:283 W: Missing Blank Line separator, <130> field identifier
 L:7 M:283 W: Missing Blank Line separator, <140> field identifier
 L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:20 M:254 E: No. of Bases conflict, LENGTH:Input:15 Counted:16 SEQ:1 ✓
 L:20 M:252 E: No. of Seq. differs, <211> LENGTH:Input:15 Found:16 SEQ:1 ✓
 L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 ✓
 L:70 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 ✓
 L:91 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8 ✓
 L:112 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10 ✓
 L:133 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12 ✓